

SEQUENCE LISTING

(1) GENERAL INFORMATION

(2) INFORMATION FOR SEQ ID NO:1:

- (A) LENGTH: 1196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(ix) **FEATURE:**

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...942
(D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

[illegible]

AGC Ser 1	TTA Leu	AAG Lys	ATG Met	ACT Thr 5	TCG Ser	AAA Lys	GTT Val	TAT Tyr	GAT Asp 10	CCA Pro	GAA Glu	CAA Gln	AGG Arg	AAA Lys 15	CGG Arg	48
ATG Met	ATA Ile	ACT Thr 20	GGT Gly	CCG Pro	CAG Gln	TGG Trp	TGG Trp	GCC Ala 25	AGA Arg	TGT Cys	AAA Lys	CAA Gln	ATG Met 30	AAT Asn	GTT Val	96
CTT Leu	GAT Asp	TCA Ser 35	TTT Phe	ATT Ile	AAT Asn	TAT Tyr 40	TAT Tyr	GAT Asp	TCA Ser	GAA Glu	AAA Lys	CAT His 45	GCA Ala	GAA Glu	AAT Asn	144
GCT Ala	GTT Val 50	ATT Ile	TTT Phe	TTA Leu	CAT His	GGT Gly 55	AAC Asn	GCG Ala	GCC Ala	TCT Ser	TCT Ser 60	TAT Tyr	TTA Leu	TGG Trp	CGA Arg	192
CAT His 65	GTT Val	GTG Val	CCA Pro	CAT His	ATT Ile 70	GAG Glu	CCA Pro	GTA Val	GCG Ala	CGG Arg 75	TGT Cys	ATT Ile	ATA Ile	CCA Pro	GAT Asp 80	240
CTT Leu	ATT Ile	GGT Gly	ATG Met 85	GGC Gly	AAA Lys	TCA Ser	GGC Gly	AAA Lys	TCT Ser 90	GGT Gly	AAT Asn	GGT Gly	TCT Ser	TAT Tyr 95	AGG Arg	288
TTA Leu	CTT Leu	GAT Asp	CAT His 100	TAC Tyr	AAA Lys	TAT Tyr	CTT Leu	ACT Thr 105	GCA Ala	TGG Trp	TTG Leu	AAC Asn	TTT Phe 110	TTA Leu	ATT Ile	336
TAC Tyr	CAA Gln 115	AGA Arg	AGA Arg	TCA Ser	TTT Phe	TTT Phe	GTC Val 120	GGC Gly	CAT His	GAT Asp	TGG Trp	GGT Gly 125	GCT Ala	TGT Cys	TTG Leu	384
GCA Ala 130	TTT Phe	CAT His	TAT Tyr	AGC Ser	TAT Tyr	GAG Glu 135	CAT His	CAA Gln	GAT Asp	AAG Lys	ATC Ile 140	AAA Lys	GCA Ala	ATA Ile	GTT Val	432
CAC His 145	GCT Ala	GAA Glu	AGT Ser	GTA Val	GTA Val 150	GAT Asp	GTG Val	ATT Ile	GAA Glu	TCA Ser 155	TGG Trp	GAT Asp	GAA Glu	TGG Trp	CCT Pro 160	480
GAT Asp	ATT Ile	GAA Glu	GAA Glu	GAT Asp 165	ATT Ile	GCG Ala	TTG Leu	ATC Ile	AAA Lys 170	TCT Ser	GAA Glu	GAA Glu	GGA Gly	GAA Glu 175	AAA Lys	528
ATG Met	GTT Val	TTG Leu	GAG Glu 180	AAT Asn	AAC Asn	TTC Phe	TTC Phe	GTG Val 185	GAA Glu	ACC Thr	ATG Met	TTG Leu	CCA Pro 190	TCA Ser	AAA Lys	576
ATC Ile	ATG Met	AGA Arg 195	AAG Lys	TTA Leu	GAA Glu	CCA Pro	GAA Glu 200	GAA Glu	TTT Phe	GCA Ala	GCA Ala	TAT Tyr 205	CTT Leu	GAA Glu	CCA Pro	624
TTC Phe	AAA Lys 210	GAG Glu	AAA Lys	GGT Gly	GAA Glu	GTT Val 215	CGT Arg	CGT Arg	CCA Pro	ACA Thr	TTA Leu 220	TCA Ser	TGG Trp	CCT Pro	CGT Arg	672
GAA Glu 225	ATC Ile	CCG Pro	TTA Leu	GTA Val	AAA Lys 230	GGT Gly	GGT Gly	AAA Lys	CCT Pro	GAC Asp 235	GTT Val	GTA Val	CAA Gln	ATT Ile	GTT Val 240	720
AGG Arg	AAT Asn	TAT Tyr	AAT Asn	GCT Ala 245	TAT Tyr	CTA Leu	CGT Arg	GCA Ala	AGT Ser 250	GAT Asp	GAT Asp	TTA Leu	CCA Pro	AAA Lys 255	ATG Met	768
TTT Phe	ATT Ile	GAA Glu	TCG Ser 260	GAT Asp	CCA Pro	GGA Gly	TTC Phe	TTT Phe 265	TCC Ser	AAT Asn	GCT Ala	ATT Ile	GTT Val 270	GAA Glu	GGC Gly	816

GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT	864
Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His	
275 280 285	
TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG	912
Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser	
290 295 300	
TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA TTACTTTTGGT TTTTATTTA	965
Phe Val Glu Arg Val Leu Lys Asn Glu Gln	
305 310	
CATTTTTCCTCC GGGTTTAATA ATATAAATGT CATTTTCAAC AATTTTATTT TAACTGAATA	1025
TTTCACAGGG AACATTCATA TATGTTGATT AATTTAGCTC GAACTTTACT CTGTCATATC	1085
ATTTTGAAT ATTACCTCTT TCAATGAAAC TTTATAAACA GTGGTTCAAT TAATTAATAT	1145
ATATTATAAT TACATTTGTT ATGTAATAAA CTCGGTTTTTA TTATAAAAAA A	1196

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1665
- (D) OTHER INFORMATION: Cypridina hilgendorffii luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: EP 0 387 355 TORAY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG AAG CTA ATA ATT CTG TCT ATT ATA TTG GCC TAC TGT GTC ACA GTC	48
Met Lys Leu Ile Ile Leu Ser Ile Ile Leu Ala Tyr Cys Val Thr Val	
1 5 10 15	
AAC TGC CAG GAT GCA TGT CCT GTA GAA GCT GAA GCA CCG TCA AGT ACA	96
Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Ala Pro Ser Ser Thr	
20 25 30	
CCA ACA GTC CCA ACA TCT TGT GAA GCT AAA GAA GGA GAA TGT ATC GAT	144
Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp	
35 40 45	
ACC AGA TGC GCA ACA TGT AAA CGA GAC ATA CTA TCA GAC GGA CTG TGT	192
Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys	
50 55 60	
GAA AAT AAA CCA GGG AAG ACA TGC TGT AGA ATG TGC CAG TAT GTA ATT	240
Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile	
65 70 75 80	
GAA TCC AGA GTA GAA GCT GCT GGA TAT TTT AGA ACG TTT TAC GCC AAA	288
Glu Ser Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Ala Lys	
85 90 95	
AGA TTT AAT TTT CAG GAA CCT GGT AAA TAT GTG CTG GCT CGA GGA ACC	336
Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr	
100 105 110	
AAG GGT GGC GAC TGG TCT GTA ACC CTC ACC ATG GAG AAT CTA GAT GGA	384
Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly	

00135990 001790

	115					120					125					
CAG Gln	AAG Lys	GGA Gly	GCT Ala	GTA Val	CTG Leu	ACT Thr	AAG Lys	ACA Thr	ACA Thr	CTG Leu	GAG Glu	GTA Val	GTA Val	GGA Gly	GAC Asp	432
	130					135					140					
GTA Val	ATA Ile	GAC Asp	ATT Ile	ACT Thr	CAA Gln	GCT Ala	ACT Thr	GCA Ala	GAT Asp	CCT Pro	ATC Ile	ACA Thr	GTT Val	AAC Asn	GGA Gly	480
145					150					155					160	
GGA Gly	GCT Ala	GAC Asp	CCA Pro	GTT Val	ATC Ile	GCT Ala	AAC Asn	CCG Pro	TTC Phe	ACA Thr	ATT Ile	GGT Gly	GAG Glu	GTG Val	ACC Thr	528
				165					170					175		
ATT Ile	GCT Ala	GTT Val	GTC Val	GAA Glu	ATA Ile	CCC Pro	GGC Gly	TTC Phe	AAT Asn	ATT Ile	ACA Thr	GTC Val	ATC Ile	GAA Glu	TTC Phe	576
			180					185					190			
TTT Phe	AAA Lys	CTA Leu	ATC Ile	GTG Val	ATA Ile	GAT Asp	ATT Ile	CTG Leu	GGA Gly	GGA Gly	AGA Arg	TCT Ser	GTG Val	AGA Arg	ATT Ile	624
		195					200					205				
GCT Ala	CCA Pro	GAC Asp	ACA Thr	GCA Ala	AAC Asn	AAA Lys	GGA Gly	CTG Leu	ATA Ile	TCT Ser	GGT Gly	ATC Ile	TGT Cys	GGT Gly	AAT Asn	672
	210					215					220					
CTG Leu	GAG Glu	ATG Met	AAT Asn	GAC Asp	GCT Ala	GAT Asp	GAC Asp	TTT Phe	ACT Thr	ACA Thr	GAC Asp	GCA Ala	GAT Asp	CAG Gln	CTG Leu	720
225					230					235					240	
GCG Ala	ATC Ile	CAA Gln	CCC Pro	AAC Asn	ATA Ile	AAC Asn	AAA Lys	GAG Glu	TTC Phe	GAC Asp	GGC Gly	TGC Cys	CCA Pro	TTC Phe	TAC Tyr	768
				245				250						255		
GGG Gly	AAT Asn	CCT Pro	TCT Ser	GAT Asp	ATC Ile	GAA Glu	TAC Tyr	TGC Cys	AAA Lys	GGT Gly	CTC Leu	ATG Met	GAG Glu	CCA Pro	TAC Tyr	816
			260					265				270				
AGA Arg	GCT Ala	GTA Val	TGT Cys	CGT Arg	AAC Asn	AAT Asn	ATC Ile	AAC Asn	TTC Phe	TAC Tyr	TAT Tyr	TAC Tyr	ACT Thr	CTG Leu	TCC Ser	864
		275					280					285				
TGC Cys	GCC Ala	TTC Phe	GCT Ala	TAC Tyr	TGT Cys	ATG Met	GGA Gly	GGA Gly	GAA Glu	GAA Glu	AGA Arg	GCT Ala	AAA Lys	CAC His	GTC Val	912
	290					295					300					
CTT Leu	TTC Phe	GAC Asp	TAT Tyr	GTT Val	GAG Glu	ACA Thr	TGC Cys	GCT Ala	GCA Ala	CCG Pro	GAA Glu	ACG Thr	AGA Arg	GGA Gly	ACG Thr	960
305				310						315					320	
TGT Cys	GTT Val	TTA Leu	TCA Ser	GGA Gly	CAT His	ACT Thr	TTC Phe	TAT Tyr	GAC Asp	ACA Thr	TTC Phe	GAC Asp	AAA Lys	GCC Ala	AGA Arg	1008
				325					330					335		
TAT Tyr	CAA Gln	TTC Phe	CAG Gln	GGC Gly	CCA Pro	TGC Cys	AAA Lys	GAG Glu	CTT Leu	CTG Leu	ATG Met	GCC Ala	GCA Ala	GAC Asp	TGT Cys	1056
			340					345					350			
TAC Tyr	TGG Trp	AAC Asn	ACA Thr	TGG Trp	GAT Asp	GTA Val	AAG Lys	GTT Val	TCA Ser	CAT His	AGA Arg	GAT Asp	GTT Val	GAG Glu	TCA Ser	1104
		355					360					365				
TAC Tyr	ACT Thr	GAG Glu	GTA Val	GAG Glu	AAA Lys	GTA Val	ACA Thr	ATC Ile	AGG Arg	AAA Lys	CAG Gln	TCA Ser	ACT Thr	GTA Val	GTA Val	1

TCT ATC CCG TAC AGT TCT GAG AAC ACA TCC ATA TAC TGG CAG GAT GGA	1248
Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly	
405 410 415	
GAC ATC CTG ACG ACG GCC ATC CTA CCT GAA GCT CTT GTC GTT AAG TTC	1296
Asp Ile Leu Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe	
420 425 430	
AAC TTT AAG CAG CTC CTT GTA GTT CAT ATC AGA GAT CCA TTC GAT GGA	1344
Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Gly	
435 440 445	
AAG ACA TGC GGC ATA TGT GGT AAC TAT AAT CAA GAT TCA ACT GAT GAT	1392
Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp	
450 455 460	
TTC TTT GAC GCA GAA GGA GCA TGC GCT CTG ACC CCC AAT CCC CCA GGA	1440
Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly	
465 470 475 480	
TGT ACA GAG GAG CAG AAA CCA GAA GCT GAG CGA CTC TGC AAT AGT CTA	1488
Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Ser Leu	
485 490 495	
TTT GAT AGT TCT ATC GAC GAG AAA TGT AAT GTC TGC TAC AAG CCT GAC	1536
Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp	
500 505 510	
CGT ATT GCA CGA TGT ATG TAC GAG TAT TGC CTG AGG GGA CAG CAA GGA	1584
Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly	
515 520 525	
TTC TGT GAC CAT GCT TGG GAG TTC AAA AAA GAA TGC TAC ATA AAG CAT	1632
Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His	
530 535 540	
GGA GAC ACT CTA GAA GTA CCA CCT GAA TGC CAA TAA ATGAACAAAG	1678
Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln	
545 550 555	
ATACAGAAGC TAAGACTACT ACAGCAGAAG ATAAAAGAGA AGCTGTAGTT CTTCAAAAAC	1738
AGTATATTTT GATGTACTCA TTGTTTACTT ACATAAAAAT AAATTGTTAT TATCATAACG	1798
TAAAGAAAAA AAAAAAAAAA AAAA	1822

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1644
- (D) OTHER INFORMATION: *Luciola Cruciata* Luciferase (Firefly)

(x) PUBLICATION INFORMATION:

PATENT NO.: 4,968,613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAA AAC ATG GAA AAC GAT GAA AAT ATT GTA GTT GGA CCT AAA CCG	48
Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Val Gly Pro Lys Pro	
1 5 10 15	

TTT	TAC	CCT	ATC	GAA	GAG	GGA	TCT	GCT	GGA	ACA	CAA	TTA	CGC	AAA	TAC	96
Phe	Tyr	Pro	Ile	Glu	Glu	Gly	Ser	Ala	Gly	Thr	Gln	Leu	Arg	Lys	Tyr	
			20					25					30			
ATG	GAG	CGA	TAT	GCA	AAA	CTT	GGC	GCA	ATT	GCT	TTT	ACA	AAT	GCA	GTT	144
Met	Glu	Arg	Tyr	Ala	Lys	Leu	Gly	Ala	Ile	Ala	Phe	Thr	Asn	Ala	Val	
		35					40					45				
ACT	GGT	GTT	GAT	TAT	TCT	TAC	GCC	GAA	TAC	TTG	GAG	AAA	TCA	TGT	TGT	192
Thr	Gly	Val	Asp	Tyr	Ser	Tyr	Ala	Glu	Tyr	Leu	Glu	Lys	Ser	Cys	Cys	
	50					55					60					
CTA	GGA	AAA	GCT	TTG	CAA	AAT	TAT	GGT	TTG	GTT	GTT	GAT	GGC	AGA	ATT	240
Leu	Gly	Lys	Ala	Leu	Gln	Asn	Tyr	Gly	Leu	Val	Val	Asp	Gly	Arg	Ile	
65					70					75					80	
GCG	TTA	TGC	AGT	GAA	AAC	TGT	GAA	GAA	TTT	TTT	ATT	CCT	GTA	ATA	GCC	288
Ala	Leu	Cys	Ser	Glu	Asn	Cys	Glu	Glu	Phe	Phe	Ile	Pro	Val	Ile	Ala	
				85					90					95		
GGA	CTG	TTT	ATA	GGT	GTA	GGT	GTT	GCA	CCC	ACT	AAT	GAG	ATT	TAC	ACT	336
Gly	Leu	Phe	Ile	Gly	Val	Gly	Val	Ala	Pro	Thr	Asn	Glu	Ile	Tyr	Thr	
			100					105					110			
TTA	CGT	GAA	CTG	GTT	CAC	AGT	TTA	GGT	ATC	TCT	AAA	CCA	ACA	ATT	GTA	384
Leu	Arg	Glu	Leu	Val	His	Ser	Leu	Gly	Ile	Ser	Lys	Pro	Thr	Ile	Val	
		115					120					125				
TTT	AGT	TCT	AAA	AAA	GGC	TTA	GAT	AAA	GTT	ATA	ACA	GTA	CAG	AAA	ACA	432
Phe	Ser	Ser	Lys	Lys	Gly	Leu	Asp	Lys	Val	Ile	Thr	Val	Gln	Lys	Thr	
	130					135					140					
GTA	ACT	ACT	ATT	AAA	ACC	ATT	GTT	ATA	CTA	GAT	AGC	AAA	GTT	GAT	TAT	480
Val	Thr	Thr	Ile	Lys	Thr	Ile	Val	Ile	Leu	Asp	Ser	Lys	Val	Asp	Tyr	
145					150					155					160	
CGA	GGA	TAT	CAA	TGT	CTG	GAC	ACC	TTT	ATA	AAA	AGA	AAC	ACT	CCA	CCA	528
Arg	Gly	Tyr	Gln	Cys	Leu	Asp	Thr	Phe	Ile	Lys	Arg	Asn	Thr	Pro	Pro	
				165					170					175		
GGT	TTT	CAA	GCA	TCC	AGT	TTC	AAA	ACT	GTG	GAA	GTT	GAC	CGT	AAA	GAA	576
Gly	Phe	Gln	Ala	Ser	Ser	Phe	Lys	Thr	Val	Glu	Val	Asp	Arg	Lys	Glu	
			180					185					190			
CAA	GTT	GCT	CTT	ATA	ATG	AAC	TCT	TCG	GGT	TCT	ACC	GGT	TTG	CCA	AAA	624
Gln	Val	Ala	Leu	Ile	Met	Asn	Ser	Ser	Gly	Ser	Thr	Gly	Leu	Pro	Lys	
		195					200					205				
GGC	GTA	CAA	CTT	ACT	CAC	GAA	AAT	ACA	GTC	ACT	AGA	TTT	TCT	CAT	GCT	672
Gly	Val	Gln	Leu	Thr	His	Glu	Asn	Thr	Val	Thr	Arg	Phe	Ser	His	Ala	
	210					215					220					
AGA	GAT	CCG	ATT	TAT	GGT	AAC	CAA	GTT	TCA	CCA	GGC	ACC	GCT	GTT	TTA	720
Arg	Asp	Pro	Ile	Tyr	Gly	Asn	Gln	Val	Ser	Pro	Gly	Thr	Ala	Val	Leu	
225					230					235					240	
ACT	GTC	GTT	CCA	TTC	CAT	CAT	GGT	TTT	GGT	ATG	TTC	ACT	ACT	CTA	GGG	768
Thr	Val	Val	Pro	Phe	His	His	Gly	Phe	Gly	Met	Phe	Thr	Thr	Leu	Gly	
				245				250						255		
TAT	TTA	ATT	TGT	GGT	TTT	CGT	GTT	GTA	ATG	TTA	ACA	AAA	TTC	GAT	GAA	816
Tyr	Leu	Ile	Cys	Gly	Phe	Arg	Val	Val	Met	Leu	Thr	Lys	Phe	Asp	Glu	
			260					265					270			
GAA	ACA	TTT	TTA	AAA	ACT	CTA	CAA	GAT	TAT	AAA	TGT	ACA	AGT	GTT	ATT	864
Glu	Thr	Phe	Leu	Lys	Thr	Leu	Gln	Asp	Tyr	Lys	Cys	Thr	Ser	Val	Ile	
		275					280					285				
CTT	GTA	CCG	ACC	TTG	TTT	GCA	ATT	CTC	AAC	AAA	AGT	GAA	TTA	CTC	AAT	912

09135999 : 091799

[illegible]

(2) INFORMATION FOR SEQ ID NO:4:

Questions **A**nswers **S**tudies **E**xercises **P**roblems **R**eview **T**est **F**inal

- (ix) FEATURE:

- (G) DATE: (1989)

ATG Met 1	AAG Lys	ATA Ile	ATA Ile	ATT Ile 5	CTG Leu	TCT Ser	GTT Val	ATA Ile	TTG Leu 10	GCC Ala	TAC Tyr	TGT Cys	GTC Val	ACC Thr 15	GAC Asp	48
AAC Asn 65	TGT Cys	CAA Gln 20	GAT Asp 20	GCA Ala	TGT Cys	CCT Pro	GTA Val	GAA Glu 25	GCG Ala	GAA Glu	CCG Pro	CCA Pro	TCA Ser 30	AGT Ser	ACA Thr	96
CCA Pro	ACA Thr 35	GTT Val 35	CCA Pro	ACT Thr	TCT Ser	TGT Cys	GAA Glu 40	GCT Ala	AAA Lys	GAA Glu	GGA Gly 45	GAA Glu 45	TGT Cys	ATA Ile	GAT Asp	144
ACC Thr 50	AGA Arg 50	TGC Cys	GCA Ala	ACA Thr	TGT Cys	AAA Lys 55	CGA Arg	GAT Asp	ATA Ile	CTA Leu 60	TCA Ser 60	GAT Asp	GGA Gly	CTG Leu	TGT Cys	192
GAA Glu 65	AAT Asn	AAA Lys	CCA Pro	GGG Gly 70	AAG Lys 70	ACA Thr	TGC Cys	TGT Cys	AGA Arg 75	ATG Met 75	TGC Cys	CAG Gln	TAT Tyr	GTG Val 80	ATT Ile 80	240
GAA Glu	TGC Cys	AGA Arg	GTA Val 85	GAA Glu 85	GCA Ala	GCT Ala	GGT Gly	TAT Tyr 90	TTT Phe 90	AGA Arg	ACG Thr	TTT Phe	TAC Tyr 95	GGC Gly 95	AAA Lys	288
AGA Arg	TTT Phe	AAT Asn 100	TTT Phe 100	CAG Gln	GAA Glu	CCT Pro	GGT Gly	AAA Lys 105	TAT Tyr	GTG Val	CTG Leu	GCT Ala 110	AGG Arg 110	GGA Gly	ACC Thr	336
AAG Lys	GGT Gly 115	GGC Gly 115	GAT Asp	TGG Trp	TCT Ser	GTA Val 120	ACC Thr 120	CTC Leu	ACC Thr	ATG Met	GAG Glu 125	AAT Asn 125	CTA Leu	GAT Asp	GGA Gly	384
CAG Gln 130	AAG Lys 130	GGA Gly	GCT Ala	GTG Val	CTG Leu	ACT Thr 135	AAG Lys 135	ACA Thr	ACA Thr	CTG Leu 140	GAG Glu 140	GTT Val	GCA Ala	GGA Gly	GAC Asp	432
GTA Val 145	ATA Ile	GAC Asp	ATT Ile	ACT Thr 150	CAA Gln 150	GCT Ala	ACT Thr	GCA Ala	GAT Asp 155	CCT Pro 155	ATC Ile	ACA Thr	GTT Val	AAC Asn 160	GGA Gly 160	480
GGA Gly	GCT Ala	GAC Asp	CCA Pro	GTT Val 165	ATC Ile	GCT Ala	AAC Asn	CCG Pro	TTC Phe 170	ACA Thr	ATT Ile	GGT Gly	GAG Glu 175	GTG Val 175	ACC Thr	528
ATT Ile	GCT Ala	GTT Val	GTT Val	GAA Glu	ATA Ile	CCG Pro	GGC Gly	TTC Phe	AAT Asn	ATC Ile	ACA Thr	GTC Val	ATC Ile	GAA Glu	TTC Phe	576

				180				185				190							
TTT	AAA	CTA	ATC	GTG	ATT	GAT	ATT	CTG	GGA	GGA	AGA	TCT	GTC	AGA	ATT	624			
Phe	Lys	Leu	Ile	Val	Ile	Asp	Ile	Leu	Gly	Gly	Arg	Ser	Val	Arg	Ile				
				195				200				205							
GCT	CCA	GAC	ACA	GCA	AAC	AAA	GGA	CTG	ATA	TCT	GGT	ATC	TGT	GGT	AAT	672			
Ala	Pro	Asp	Thr	Ala	Asn	Lys	Gly	Leu	Ile	Ser	Gly	Ile	Cys	Gly	Asn				
				210				215				220							
CTG	GAG	ATG	AAT	GAC	GCT	GAT	GAC	TTT	ACT	ACA	GAT	GCA	GAT	CAG	CTG	720			
Leu	Glu	Met	Asn	Asp	Ala	Asp	Asp	Phe	Thr	Thr	Asp	Ala	Asp	Gln	Leu				
				225				230				235				240			
GCG	ATC	CAA	CCC	AAC	ATA	AAC	AAA	GAG	TTC	GAC	GGC	TGC	CCA	TTC	TAT	768			
Ala	Ile	Gln	Pro	Asn	Ile	Asn	Lys	Glu	Phe	Asp	Gly	Cys	Pro	Phe	Tyr				
				245				250				255							
GGC	AAT	CCT	TCT	GAT	ATC	GAA	TAC	TGC	AAA	GGT	CTG	ATG	GAG	CCA	TAC	816			
Gly	Asn	Pro	Ser	Asp	Ile	Glu	Tyr	Cys	Lys	Gly	Leu	Met	Glu	Pro	Tyr				
				260				265				270							
AGA	GCT	GTA	TGT	CGT	AAC	AAT	ATC	AAC	TTC	TAC	TAT	TAC	ACT	CTA	TCC	864			
Arg	Ala	Val	Cys	Arg	Asn	Asn	Ile	Asn	Phe	Tyr	Tyr	Tyr	Thr	Leu	Ser				
				275				280				285							
TGT	GCC	TTC	GCT	TAC	TGT	ATG	GGA	GGA	GAA	GAA	AGA	GCT	AAA	CAC	GTC	912			
Cys	Ala	Phe	Ala	Tyr	Cys	Met	Gly	Gly	Glu	Glu	Arg	Ala	Lys	His	Val				
				290				295				300							
CTT	TTC	GAC	TAT	GTT	GAG	ACA	TGC	GCT	GCG	CCG	GAA	ACG	AGA	GGA	ACG	960			
Leu	Phe	Asp	Tyr	Val	Glu	Thr	Cys	Ala	Ala	Pro	Glu	Thr	Arg	Gly	Thr				
				305				310				315				320			
TGT	GTT	TTA	TCA	GGA	CAT	ACT	TTC	TAT	GAC	ACA	TTC	GAC	AAA	GCA	AGA	1008			
Cys	Val	Leu	Ser	Gly	His	Thr	Phe	Tyr	Asp	Thr	Phe	Asp	Lys	Ala	Arg				
				325				330				335							
TAT	CAA	TTC	CAG	GGC	CCA	TGC	AAG	GAG	ATT	CTG	ATG	GCC	GCA	GAC	TGT	1056			
Tyr	Gln	Phe	Gln	Gly	Pro	Cys	Lys	Glu	Ile	Leu	Met	Ala	Ala	Asp	Cys				
				340				345				350							
TAC	TGG	AAC	ACA	TGG	GAT	GTA	AAG	GTT	TCA	CAT	AGA	GAC	GTC	GAA	TCA	1104			
Tyr	Trp	Asn	Thr	Trp	Asp	Val	Lys	Val	Ser	His	Arg	Asp	Val	Glu	Ser				
				355				360				365							
TAC	ACT	GAG	GTA	GAG	AAA	GTA	ACA	ATC	AGG	AAA	CAG	TCA	ACT	GTA	GTA	1152			
Tyr	Thr	Glu	Val	Glu	Lys	Val	Thr	Ile	Arg	Lys	Gln	Ser	Thr	Val	Val				
				370				375				380							
GAT	CTC	ATT	GTG	GAT	GGC	AAG	CAG	GTC	AAG	GTT	GGA	GGA	GTG	GAT	GTA	1200			
Asp	Leu	Ile	Val	Asp	Gly	Lys	Gln	Val	Lys	Val	Gly	Gly	Val	Asp	Val				
				385				390				395				400			
TCT	ATC	CCG	TAC	AGC	TCT	GAG	AAC	ACT	TCC	ATA	TAC	TGG	CAG	GAT	GGA	1248			
Ser	Ile	Pro	Tyr	Ser	Ser	Glu	Asn	Thr	Ser	Ile	Tyr	Trp	Gln	Asp	Gly</				

TTC TTT GAC GCA GAA GGA GCA TGC GCT CTA ACC CCC AAC CCC CCA GGA 1440
 Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly
 465 470 475 480
 TGT ACA GAG GAA CAG AAA CCA GAA GCT GAG CGA CTT TGC AAT AAT CTC 1488
 Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Asn Leu
 485 490 495
 TTT GAT TCT TCT ATC GAC GAG AAA TGT AAT GTC TGC TAC AAG CCT GAC 1536
 Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp
 500 505 510
 CGG ATT GCC CGA TGT ATG TAC GAG TAT TGC CTG AGG GGA CAA CAA GGA 1584
 Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly
 515 520 525
 TTT TGT GAC CAT GCT TGG GAG TTC AAG AAA GAA TGC TAC ATA AAA CAT 1632
 Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His
 530 535 540
 GGA GAC ACT CTA GAA GTA CCA CCT GAA TGT CAA TAA ACGTACAAAG 1678
 Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln
 545 550 555
 ATACAGAAGC TAAGGCTACT ACAGCAGAAG ATAAAAAAGA AACTGTAGTT CCTTCAAAAA 1738
 CCGTGTATTT TATGTACTCA TTGTTTAATT AGAGCAAAAT AAATTGTTAT TATCATAACT 1798
 TAACTAAAA AAAAAAAAAA AA 1820

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 115...702
- (D) OTHER INFORMATION: apoaeguorin-encoding gene

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,093,240

(A) AUTHORS: Inouye *et al.*

(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

(D) VOLUME: 82

(F) PAGES: 3154-3158

(G) DATE: (1985)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGAATGCAA TTCATCTTTG CATCAAAGAA 60
 TTACATCAAA TCTCTAGTTG ATCAACTAAA TTGTCTCGAC AACACAAGC AAAC ATG 117
 Met
 1
 ACA AGC AAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC CCA 165
 Thr Ser Lys Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn Pro
 5 10 15
 AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC AAC 213
 Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val Asn

20				25				30									
CAC His	AAT Asn 35	GGA Gly	AAA Lys	ATC Ile	TCT Ser	CTT Leu 40	GAC Asp	GAG Glu	ATG Met	GTC Val	TAC Tyr 45	AAG Lys	GCA Ala	TCT Ser	GAT Asp	261	
ATT Ile 50	GTC Val	ATC Ile	AAT Asn	AAC Asn	CTT Leu 55	GGA Gly	GCA Ala	ACA Thr	CCT Pro	GAG Glu 60	CAA Gln	GCC Ala	AAA Lys	CGA Arg	CAC His 65	309	
AAA Lys	GAT Asp	GCT Ala	GTA Val	GAA Glu 70	GCC Ala	TTC Phe	TTC Phe	GGA Gly	GGA Gly 75	GCT Ala	GGA Gly	ATG Met	AAA Lys	TAT Tyr 80	GGT Gly	357	
GTG Val	GAA Glu	ACT Thr	GAT Asp 85	TGG Trp	CCT Pro	GCA Ala	TAT Tyr	ATT Ile 90	GAA Glu	GGA Gly	TGG Trp	AAA Lys	AAA Lys 95	TTG Leu	GCT Ala	405	
ACT Thr	GAT Asp	GAA Glu 100	TTG Leu	GAG Glu	AAA Lys	TAC Tyr	GCC Ala 105	AAA Lys	AAC Asn	GAA Glu	CCA Pro	ACG Thr 110	CTC Leu	ATC Ile	CGT Arg	453	
ATA Ile 115	TGG Trp	GGT Gly	GAT Asp	GCT Ala	TTG Leu	TTT Phe 120	GAT Asp	ATC Ile	GTT Val	GAC Asp	AAA Lys 125	GAT Asp	CAA Gln	AAT Asn	GGA Gly	501	
GCC Ala 130	ATT Ile	ACA Thr	CTG Leu	GAT Asp	GAA Glu 135	TGG Trp	AAA Lys	GCA Ala	TAC Tyr	ACC Thr 140	AAA Lys	GCT Ala	GCT Ala	GGT Gly	ATC Ile 145	549	
ATC Ile	CAA Gln	TCA Ser	TCA Ser	GAA Glu 150	GAT Asp	TGC Cys	GAG Glu	GAA Glu	ACA Thr 155	TTC Phe	AGA Arg	GTG Val	TGC Cys	GAT Asp 160	ATT Ile	597	
GAT Asp	GAA Glu	AGT Ser	GGA Gly 165	CAA Gln	CTC Leu	GAT Asp	GTT Val 170	GAT Glu	GAG Glu	ATG Met	ACA Thr	AGA Arg	CAA Gln 175	CAT His	TTA Leu	645	
GGA Gly	TTT Phe 180	TGG Trp	TAC Tyr	ACC Thr	ATG Met	GAT Asp	CCT Pro 185	GCT Ala	TGC Cys	GAA Glu	AAG Lys	CTC Leu 190	TAC Tyr	GGT Gly	GGA Gly	693	
GCT Ala 195	GTC Val	CCC Pro	TAAGAAGCTC			TACGGTGGTG			ATGCACCCTA			GGAAGATGAT			GTGATTTTGA		752
ATAAAACACT			GATGAATTCA			ATCAAAATTT			TCCAAATTTT			TGAACGATTT			CAATCGTTTG		812
TGTTGATTTT			TGTAATTAGG			AACAGATTAA			ATCGAATGAT			TAGTTGTTTT			TTTAATCAAC		872
AGAACTTACA			AATCGAAAAA			GTAAAAAAA			AAAAAAA			AAAAAAA			AAAAAAA		932
AAAAAAAAA			AAAAAAAAA			AAAAA											958

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) **FEATURE:**

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...588
(D) OTHER INFORMATION: Recombinant Aequorin AEQ1

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Prasher et al.
(B) TITLE: Sequence Comparisons of Complementary
DNAs Encoding Aequorin Isotypes
(C) JOURNAL: Biochemistry
(D) VOLUME: 26
(F) PAGES: 1326-1332
(G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn	
1 5 10 15	
CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC	96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC	144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr	
65 70 75 80	
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG	288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu	
85 90 95	
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT	336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile	
100 105 110	
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT GAC AAA GAC CAA AAT	384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Asp Lys Asp Gln Asn	
115 120 125	
GGA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GAT GGC	432
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Asp Gly	
130 135 140	
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp	
145 150 155 160	
ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	
GGA GCT GTC CCC TAA	591
Gly Ala Val Pro *	
195	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 591 base pairs

09135999 091799

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:
```

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...588
(D) OTHER INFORMATION: Recombinant Aequorin AEQ2

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Prasher et al.
(B) TITLE: Sequence Comparisons of Complementary
DNAs Encoding Aequorin Isotypes
(C) JOURNAL: Biochemistry
(D) VOLUME: 26
(F) PAGES: 1326-1332
(G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG Met 1	ACC Thr	AGC Ser	GAA Glu	CAA Gln 5	TAC Tyr	TCA Ser	GTC Val	AAG Lys	CTT Leu 10	ACA Thr	TCA Ser	GAC Asp	TTC Phe 15	GAC Asp	AAC Asn	48
CCA Pro 65	AGA Arg	TGG Trp	ATT Ile 20	GGA Gly	CGA Arg	CAC His	AAG Lys	CAT His 25	ATG Met	TTC Phe	AAT Asn	TTC Phe	CTT Leu 30	GAT Asp	GTC Val	96
AAC Asn	CAC His	AAT Asn 35	GGA Gly	AAA Lys	ATC Ile	TCT Ser	CTT Leu 40	GAC Asp	GAG Glu	ATG Met	GTC Val	TAC Tyr 45	AAG Lys	GCA Ala	TCT Ser	144
GAT Asp 50	ATT Ile	GTC Val	ATC Ile	AAT Asn	AAC Asn	CTT Leu 55	GGA Gly	GCA Ala	ACA Thr	CCT Pro	GAG Glu 60	CAA Gln	GCC Ala	AAA Lys	CGA Arg	192
CAC His 65	AAA Lys	GAT Asp	GCT Ala	GTA Val	GAA Glu 70	GCC Ala	TTC Phe	TTC Phe	GGA Gly 75	GGA Gly	GCT Ala	GGA Gly	ATG Met	AAA Lys	TAT Tyr 80	240
GGT Gly	GTG Val	GAA Glu	ACT Thr	GAT Asp 85	TGG Trp	CCT Pro	GCA Ala	TAT Tyr	ATT Ile 90	GAA Glu	GGA Gly	TGG Trp	AAA Lys 95	AAA Lys	TTG Leu	288
GCT Ala	ACT Thr	GAT Asp	GAA Glu 100	TTG Leu	GAG Glu	AAA Lys	TAC Tyr	GCC Ala 105	AAA Lys	AAC Asn	GAA Glu	CCA Pro	ACG Thr 110	CTC Leu	ATC Ile	336
CGT Arg	ATA Ile	TGG Trp 115	GGT Gly	GAT Asp	GCT Ala	TTG Leu	TTC Phe 120	GAT Asp	ATC Ile	GTT Val	GAC Asp	AAA Lys 125	GAT Asp	CAA Gln	AAT Asn	384
GGA Gly 130	GCC Ala	ATT Ile	ACA Thr	CTG Leu	GAT Asp	GAA Glu 135	TGG Trp	AAA Lys	GCA Ala	TAC Tyr	ACC Thr 140	AAA Lys	GCT Ala	GCT Ala	GGT Gly	432
ATC Ile 145	ATC Ile	CAA Gln	TCA Ser	TCA Ser	GAA Glu 150	GAT Asp	TGC Cys	GAG Glu	GAA Glu	ACA Thr 155	TTC Phe	AGA Arg	GTG Val	TGC Cys	GAT Asp 160	480
ATT Ile	GAT Asp	GAA Glu	AGT Ser	GGA Gly	CAA Gln	CTC Leu	GAT Asp	GTT Val	GAT Asp	GAG Glu	ATG Met	ACA Thr	AGA Arg	CAA Gln	CAT His	528

	165		170		175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT						576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly						
	180		185		190	
GGA GCT GTC CCC TAA						591
Gly Ala Val Pro *						
	195					

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...588
- (D) OTHER INFORMATION: Recombinant Aequorin AEQ3

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Prasher et al.
- (B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isotypes
- (C) JOURNAL: Biochemistry
- (D) VOLUME: 26
- (F) PAGES: 1326-1332
- (G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn	
1 5 10 15	
CCA AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC	96
Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT	144
Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GGA GAC TTC TTC GGA GGA GCT GGA ATG AAA TAT	240
His Lys Asp Ala Val Gly Asp Phe Phe Gly Gly Ala Gly Met Lys Tyr	
65 70 75 80	
GGT GTG GAA ACT GAT TGG CCT GCA TAC ATT GAA GGA TGG AAA AAA TTG	288
Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu	
85 90 95	
GCT ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC	336
Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile	
100 105 110	

CGT	ATA	TGG	GGT	GAT	GCT	TTG	TTC	GAT	ATC	GTT	GAC	AAA	GAT	CAA	AAT	384
Arg	Ile	Trp	Gly	Asp	Ala	Leu	Phe	Asp	Ile	Val	Asp	Lys	Asp	Gln	Asn	
		115					120					125				
GGA	GCC	ATT	ACA	CTG	GAT	GAA	TGG	AAA	GCA	TAC	ACC	AAA	GCT	GCT	GGT	432
Gly	Ala	Ile	Thr	Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ala	Ala	Gly	
		130					135				140					
ATC	ATC	CAA	TCA	TCA	GAA	GAT	TGC	GAG	GAA	ACA	TTC	AGA	GTG	TGC	GAT	480
Ile	Ile	Gln	Ser	Ser	Glu	Asp	Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	
					150					155					160	
ATT	GAT	GAA	AAT	GGA	CAA	CTC	GAT	GTT	GAT	GAG	ATG	ACA	AGA	CAA	CAT	528
Ile	Asp	Glu	Asn	Gly	Gln	Leu	Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His	
				165					170						175	
TTA	GGA	TTT	TGG	TAC	ACC	ATG	GAT	CCT	GCT	TGC	GAA	AAG	CTC	TAC	GGT	576
Leu	Gly	Phe	Trp	Tyr	Thr	Met	Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly	
			180					185					190			
GGA	GCT	GTC	CCC	TAA												591
Gly	Ala	Val	Pro	*												
			195													

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...567
- (D) OTHER INFORMATION: Aequorin photoprotein

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Charbonneau et al.
- (B) TITLE: Amino acid sequence of the calcium-dependent photoprotein aequorin
- (C) JOURNAL: Am. Chem. Soc.
- (D) VOLUME: 24
- (E) ISSUE: 24
- (F) PAGES: 6762-6771
- (G) DATE: 1985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTC	AAG	CTT	ACA	CCA	GAC	TTC	GAC	AAC	CCA	AAA	TGG	ATT	GGA	CGA	CAC	48
Val	Lys	Leu	Thr	Pro	Asp	Phe	Asp	Asn	Pro	Lys	Trp	Ile	Gly	Arg	His	
1				5				10						15		
AAG	CAC	ATG	TTT	AAT	TTT	CTT	GAT	GTC	AAC	CAC	AAT	GGA	AGG	ATC	TCT	96
Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	Asn	His	Asn	Gly	Arg	Ile	Ser	
			20					25				30				
CTT	GAC	GAG	ATG	GTC	TAC	AAG	GCG	TCC	GAT	ATT	GTT	ATA	AAC	AAT	CTT	144
Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	Asp	Ile	Val	Ile	Asn	Asn	Leu	
		35					40					45				

Biochem Biophys Res Commun

GGA	GCA	ACA	CCT	GAA	CAA	GCC	AAA	CGT	CAC	AAA	GAT	GCT	GTA	GAA	GCC	192
Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	His	Lys	Asp	Ala	Val	Glu	Ala	
	50					55					60					
TTC	TTC	GGA	GGA	GCT	GCA	ATG	AAA	TAT	GGT	GTA	GAA	ACT	GAA	TGG	CCT	240
Phe	Phe	Gly	Gly	Ala	Ala	Met	Lys	Tyr	Gly	Val	Glu	Thr	Glu	Trp	Pro	
65					70					75					80	
GAA	TAC	ATC	GAA	GGA	TGG	AAA	AGA	CTG	GCT	TCC	GAG	GAA	TTG	AAA	AGG	288
Glu	Tyr	Ile	Glu	Gly	Trp	Lys	Arg	Leu	Ala	Ser	Glu	Glu	Leu	Lys	Arg	
				85					90					95		
TAT	TCA	AAA	AAC	CAA	ATC	ACA	CTT	ATT	CGT	TTA	TGG	GGT	GAT	GCA	TTG	336
Tyr	Ser	Lys	Asn	Gln	Ile	Thr	Leu	Ile	Arg	Leu	Trp	Gly	Asp	Ala	Leu	
			100					105					110			
TTC	GAT	ATC	ATT	GAC	AAA	GAC	CAA	AAT	GGA	GCT	ATT	TCA	CTG	GAT	GAA	384
Phe	Asp	Ile	Ile	Asp	Lys	Asp	Gln	Asn	Gly	Ala	Ile	Ser	Leu	Asp	Glu	
			115				120					125				
TGG	AAA	GCA	TAC	ACC	AAA	TCT	GCT	GGC	ATC	ATC	CAA	TCG	TCA	GAA	GAT	432
Trp	Lys	Ala	Tyr	Thr	Lys	Ser	Ala	Gly	Ile	Ile	Gln	Ser	Ser	Glu	Asp	
	130					135					140					
TGC	GAG	GAA	ACA	TTC	AGA	GTG	TGC	GAT	ATT	GAT	GAA	AGT	GGA	CAG	CTC	480
Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	Ile	Asp	Glu	Ser	Gly	Gln	Leu	
145					150					155					160	
GAT	GTT	GAT	GAG	ATG	ACA	AGA	CAA	CAT	TTA	GGA	TTT	TGG	TAC	ACC	ATG	528
Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His	Leu	Gly	Phe	Trp	Tyr	Thr	Met	
				165					170					175		
GAT	CCT	GCT	TGC	GAA	AAG	CTC	TAC	GGT	GGA	GCT	GTC	CCC				567
Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly	Gly	Ala	Val	Pro				
			180					185								

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Aequorin mutant w/increased bioluminescence activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO: 10:

Asp 124 changed to Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG	ACC	AGC	GAA	CAA	TAC	TCA	GTC	AAG	CTT	ACA	CCA	GAC	TTC	GAC	AAC	48
Met	Thr	Ser	Glu	Gln	Tyr	Ser	Val	Lys	Leu	Thr	Pro	Asp	Phe	Asp	Asn	
1				5					10					15		

CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC	96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC	144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr	
65 70 75 80	
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG	288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu	
85 90 95	
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT	336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile	
100 105 110	
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT	384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn	
115 120 125	
GGA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GCT GGC	432
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly	
130 135 140	
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp	
145 150 155 160	
ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	
GGA GCT GTC CCC	588
Gly Ala Val Pro	
195	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Recombinant site-directed Aequorin mutant w/increased biolum. activity

[illegible]

588

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...567
- (D) OTHER INFORMATION: Recombinant apoaeguorin (AQUALITE®)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTC	AAG	CTT	ACA	CCA	GAC	TTC	GAC	AAC	CCA	AAA	TGG	ATT	GGA	CGA	CAC	48
Val	Lys	Leu	Thr	Pro	Asp	Phe	Asp	Asn	Pro	Lys	Trp	Ile	Gly	Arg	His	
1				5					10					15		
AAG	CAC	ATG	TTT	AAT	TTT	CTT	GAT	GTC	AAC	CAC	AAT	GGA	AGG	ATC	TCT	96
Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	Asn	His	Asn	Gly	Arg	Ile	Ser	
			20					25					30			
CTT	GAC	GAG	ATG	GTC	TAC	AAG	GCG	TCC	GAT	ATT	GTT	ATA	AAC	AAT	CTT	144
Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	Asp	Ile	Val	Ile	Asn	Asn	Leu	
		35					40					45				
GGA	GCA	ACA	CCT	GAA	CAA	GCC	AAA	CGT	CAC	AAA	GAT	GCT	GTA	GAA	GCC	192
Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	His	Lys	Asp	Ala	Val	Glu	Ala	
	50					55					60					
TTC	TTC	GGA	GGA	GCT	GGA	ATG	AAA	TAT	GGT	GTA	GAA	ACT	GAA	TGG	CCT	240
Phe	Phe	Gly	Gly	Ala	Gly	Met	Lys	Tyr	Gly	Val	Glu	Thr	Glu	Trp	Pro	
65					70				75						80	
GAA	TAC	ATC	GAA	GGA	TGG	AAA	AAA	CTG	GCT	TCC	GAG	GAA	TTG	AAA	AGG	288
Glu	Tyr	Ile	Glu	Gly	Trp	Lys	Lys	Leu	Ala	Ser	Glu	Glu	Leu	Lys	Arg	
				85				90						95		
TAT	TCA	AAA	AAC	CAA	ATC	ACA	CTT	ATT	CGT	TTA	TGG	GGT	GAT	GCA	TTG	336
Tyr	Ser	Lys	Asn	Gln	Ile	Thr	Leu	Ile	Arg	Leu	Trp	Gly	Asp	Ala	Leu	
			100					105					110			
TTC	GAT	ATC	ATT	GAC	AAA	GAC	CAA	AAT	GGA	GCT	ATT	CTG	TCA	GAT	GAA	384
Phe	Asp	Ile	Ile	Asp	Lys	Asp	Gln	Asn	Gly	Ala	Ile	Leu	Ser	Asp	Glu	
		115					120					125				
TGG	AAA	GCA	TAC	ACC	AAA	TCT	GAT	GGC	ATC	ATC	CAA	TCG	TCA	GAA	GAT	432
Trp	Lys	Ala	Tyr	Thr	Lys	Ser	Asp	Gly	Ile	Ile	Gln	Ser	Ser	Glu	Asp	
	130					135					140					
TGC	GAG	GAA	ACA	TTC	AGA	GTG	TGC	GAT	ATT	GAT	GAA	AGT	GGA	CAG	CTC	480
Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	Ile	Asp	Glu	Ser	Gly	Gln	Leu	
145					150				155					160		
GAT	GTT	GAT	GAG	ATG	ACA	AGA	CAA	CAT	TTA	GGA	TTT	TGG	TAC	ACC	ATG	528
Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His	Leu	Gly	Phe	Trp	Tyr	Thr	Met	
				165				170						175		
GAT	CCT	GCT	TGC	GAA	AAG	CTC	TAC	GGT	GGA	GCT	GTC	CCC				567
Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly	Gly	Ala	Val	Pro				
			180					185								

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x) PUBLICATION INFORMATION:
PATENT NO.: 5,484,723

(ix) FEATURE:

(D) OTHER INFORMATION: Vibrio fisheri Flavín reductase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Pro Ile Asn Cys Lys Val Lys Ser Ile Glu Pro Leu Ala Cys Asn
1 5 10 15
Thr Phe Arg Ile Leu Leu His Pro Glu Gln Pro Val Ala Phe Lys Ala
20 25 30
Gly Gln Tyr Leu Thr Val Val Met Gly Glu Lys Asp Lys Arg Pro Phe
35 40 45
Ser Ile Ala Ser Ser Pro Cys Arg His Glu Gly Glu Ile Glu Leu His
50 55 60
Ile Gly Ala Ala Glu His Asn Ala Tyr Ala Gly Glu Val Val Glu Ser
65 70 75 80
Met Lys Ser Ala Leu Glu Thr Gly Gly Asp Ile Leu Ile Asp Ala Pro
85 90 95
His Gly Glu Ala Trp Ile Arg Glu Asp Ser Asp Arg Ser Met Leu Leu
100 105 110
Ile Ala Gly Gly Thr Gly Phe Ser Tyr Val Arg Ser Ile Leu Asp His
115 120 125
Cys Ile Ser Gln Gln Ile Gln Lys Pro Ile Tyr Leu Tyr Trp Gly Gly
130 135 140
Arg Asp Glu Cys Gln Leu Tyr Ala Lys Ala Glu Leu Glu Ser Ile Ala
145 150 155 160
Gln Ala His Ser His Ile Thr Phe Val Pro Val Val Glu Lys Ser Glu
165 170 175
Gly Trp Thr Gly Lys Thr Gly Asn Val Leu Glu Ala Val Lys Ala Asp
180 185 190
Phe Asn Ser Leu Ala Asp Met Asp Ile Tyr Ile Ala Gly Arg Phe Glu
195 200 205
Met Ala Gly Ala Ala Arg Glu Gln Phe Thr Thr Glu Lys Gln Ala Lys
210 215 220
Lys Glu Gln Leu Phe Gly Asp Ala Phe Ala Phe Ile
225 230 235

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